



Fig.1

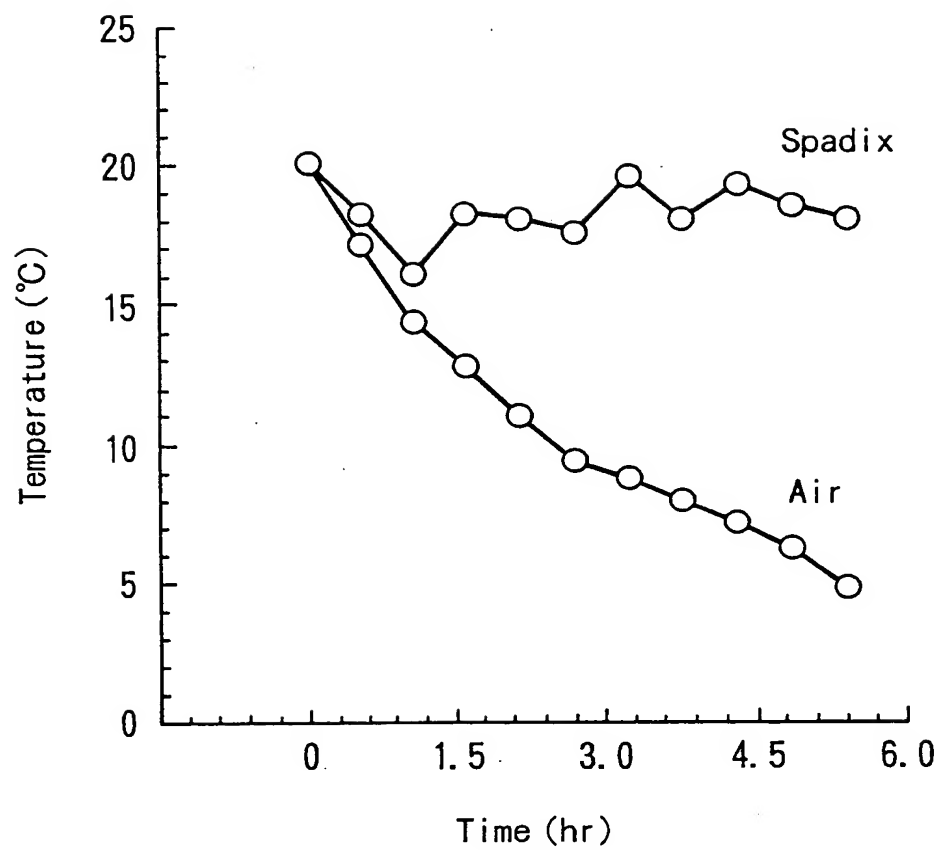


Fig.2

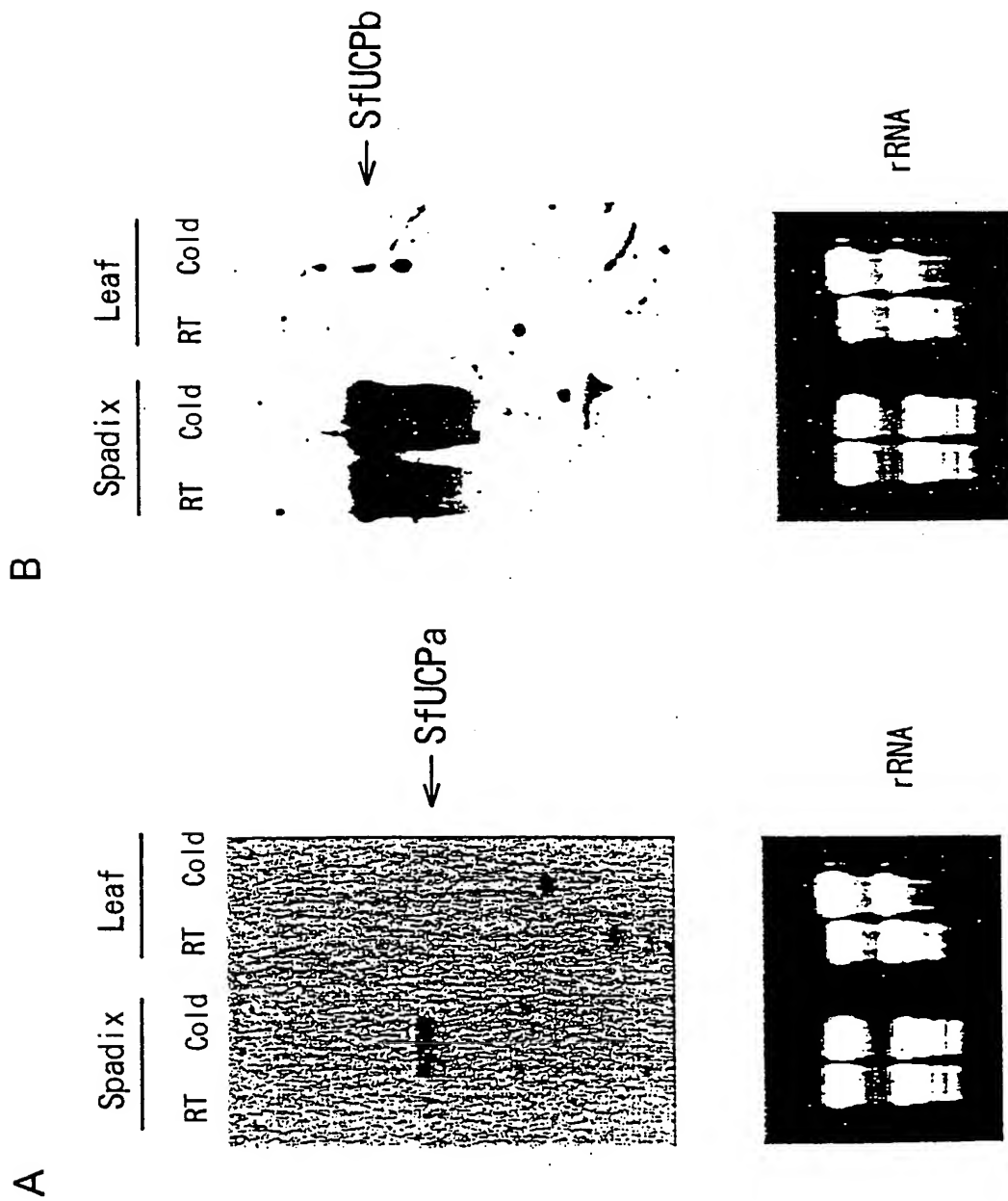


Fig.3 Top

I

SfUCPA	1	--MGD	HGPRTEISFAGSSR-AAFAACFAELCTI	PLDTAKVRILQLQKRAVTGDV-VALPKY	56
SfUCPB	1	--MGD	HGPRTEISFAGSSR-AAFAACFAELCTI	PLDTAKVRILQLQKRAVTGDV-VALPKY	56
StUCP	1	MGG	DHGKSDISFAGIFASSAFAACFAEACTI	PLDTAKVRILQLQKRAVEGDG-LALPKY	59
AtPUMP	1	---	MVAACKSOLSLPKTFACSAFAACVGEVCTI	PLDTAKVRILQLQKSAFTLAGDVTLPKY	57
human UCP1	1	-MG	GLTASDVHPTLGVQLFSAPIAACLADVIT	PLDTAKVRILQVQGECP-----TSSVIRY	55
human UCP2	1	-MV	GFKATDVPPATATVKFLGAGTAACIADLIT	PLDTAKVRILQIQGESQCPVRATASAOY	59
human UCP3	1	-MV	GLKPSDVPPPTMAVKFLGAGTAACFADLV	PLDTAKVRILQIQGENQ-AVQTARLVQY	58

II

SfUCPA	57	RGMLG	TVATIAREEGLSALWKGIVPGLHRQCLF	CGGLRIGLYEPVKSFYVG--DNFVGDIP	114
SfUCPB	57	RGMLG	TVATIAREEGLSALWKGIVPGLHRQCLF	CGGLRIGLYEPVKSFYVG--DNFVGDIP	114
StUCP	60	RGLLG	TVGTIAKEEGLASLWKGIVPGLHRQCI	YGGLRIGHYEPVKNLVYG--KDHVGDVP	117
AtPUMP	58	RGLLG	TVGTIAREEGLRSLWKGIVPGLHRQCLF	CGGLRIGMYEPVKNLVYFTGKDFVGDVP	117
human UCP1	56	KGVLG	TITAVVKTEGRMKLYSGLPAGLQRQIS	SASLRIGLYDVTVQEFFLTA---GKETAPS	112
human UCP2	60	RGVMG	TILTMVRTEGPRSLYNGLVAGLQRQMS	FASVRIGLYDSVKQFYT-----KGSEHAS	115
human UCP3	59	RGVLG	TILTMVRTEGPCSPYNGLVAGLQRQMS	FASIRIGLYDSVKQVYTP---KGADNSS	115

Fig.3 Middle

III

SfUCPA	115	LSKKILAGLTGALAIIVANPTDLVKVRLQSEGKLPAG--VPRRYSGALNAY--STIVKRE	171
SfUCPB	115	LSKKILAGLTGALAIIVANPTDLVKVRLQSEGKLPAG--VPRRYSGALNAY--STIVKRE	171
StUCP	118	LSKKILAAALTGALGITIANPTDLVKVRLQAEGLPAG--VPRRYSGALNAY--STIVKQE	174
AtPUMP	118	LSKKILAGLTGALGIMVANPTDLVKVRLQAEGLAAG--APRRYSGALNAYFTSTIVRQE	176
human UCP1	113	LGSKILAGLTGAVFICQPTDVVKVRLQAQSHLHG--IKPRYTGTYNAY--RIIATTE	168
human UCP2	116	IGSRLLAGSTGALAVACQPTDVVKVRFQAQARAG---GGRRYQSTVNAY--KTIAREE	170
human UCP3	116	LTTRILAGCTTGAMAVTCAQPTDVVKVRFQASIHLPSSDRKYSGTMDAY--RTIAREE	173
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IV

SfUCPA	172	GLGALHTGLGPNIARNAIINAAELASYDQVKQTIKLPGFSDNIFTHILAG--LGAGFFA	229
SfUCPB	172	GLGALHTGLGPNIARNAIINAAELASYDQVKQ-----	203
StUCP	175	GVRALWTGLGPNICRNAIINAAELASYDQVKEAVLRIPGFTDNVVTHTLIAG--LGAGFFA	232
AtPUMP	177	GVRALWTVLGPVNARNAIINAAELASYDQVKETILKIPGFTDNVVTHTILSGLFTGAGFFA	236
human UCP1	169	GLTGLWKGTTPNLMRSVIINCTELVTYDLMKEAFVKNNILADDDVPCHLVA--LIAGFCA	226
human UCP2	171	GFRGLWKGTSPNVARNAIIVNCAELVTYDLIKDALLKANLMTDOLPCHFTSA--FGAGFCT	228
human UCP3	174	GVRGLWKGTLPNIMRNAIIVNCAEVVTTYDILKEKLLDYHLLTDNFPCHFVSA--FGAGFCA	231
		*..**.. ***..*..*..*..*..*..*..*	

V

Fig.3 Down

VI

SfUCPA	230	VCIGSPVDVVKSRM	MGDS---	AYKSTFDCF	IKILKNDG	LLAFYKGF	IPNFGR	LG---	SWNVI	285
SfUCPB	204	-----	MKSRM	MGDS---	AYKSTFDCF	IKILKNDG	PLAFYKGF	IPNFGR	LG---	SWNVI
StUCP	233	VCIGSPVDVVKSRM	MGDS---	AYKNTLDC	FVKTLKNDG	PLAFYKGF	IPNFGR	LG---	SWNVI	288
AtPUMP	237	VCIGSPVDVVKSRM	MGDS-	AYKGTIDC	FVKTLKSDG	PMAFYKGF	IPNFGR	LGSTW	NVI	295
human UCP1	227	TAMSSPVDVVKTRH	INSPPGQYK	SVFNCAMKV	FTNEGPTA	FKGLVP	SFLRLG	---	SWNVI	284
human UCP2	229	TVIASPVDVVKTRH	MNSALGQYSS	AGHCAL	TMLQKEG	PPRAF	YKGFMP	SFLRLG	---	SWNVV
human UCP3	232	TVVASPVDVVKTRH	MNSPBGQYFS	P2LDCMIK	MAQEGPTA	FKGFTP	SFLRLG	---	SWNVV	289

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PNBD

SfUCPA	286	MFLTLEQVKKFF	IKVFN-----	303
SfUCPB	251	MFLTLEQVKKFF	IKVFN-----	268
StUCP	289	MFLTLEQAKKFVKS	LESP-----	306
AtPUMP	296	MFLTLEQAKKYVRE	LDAKRN--	316
human UCP1	285	MFVCFEQKREL	SKSRQTHDCAT	307
human UCP2	289	MFVTTYEQKRAL	MAACTSREAPF	309
human UCP3	290	MFVTTYEQKRAL	MKVQMLRESPP	312

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Fig.4

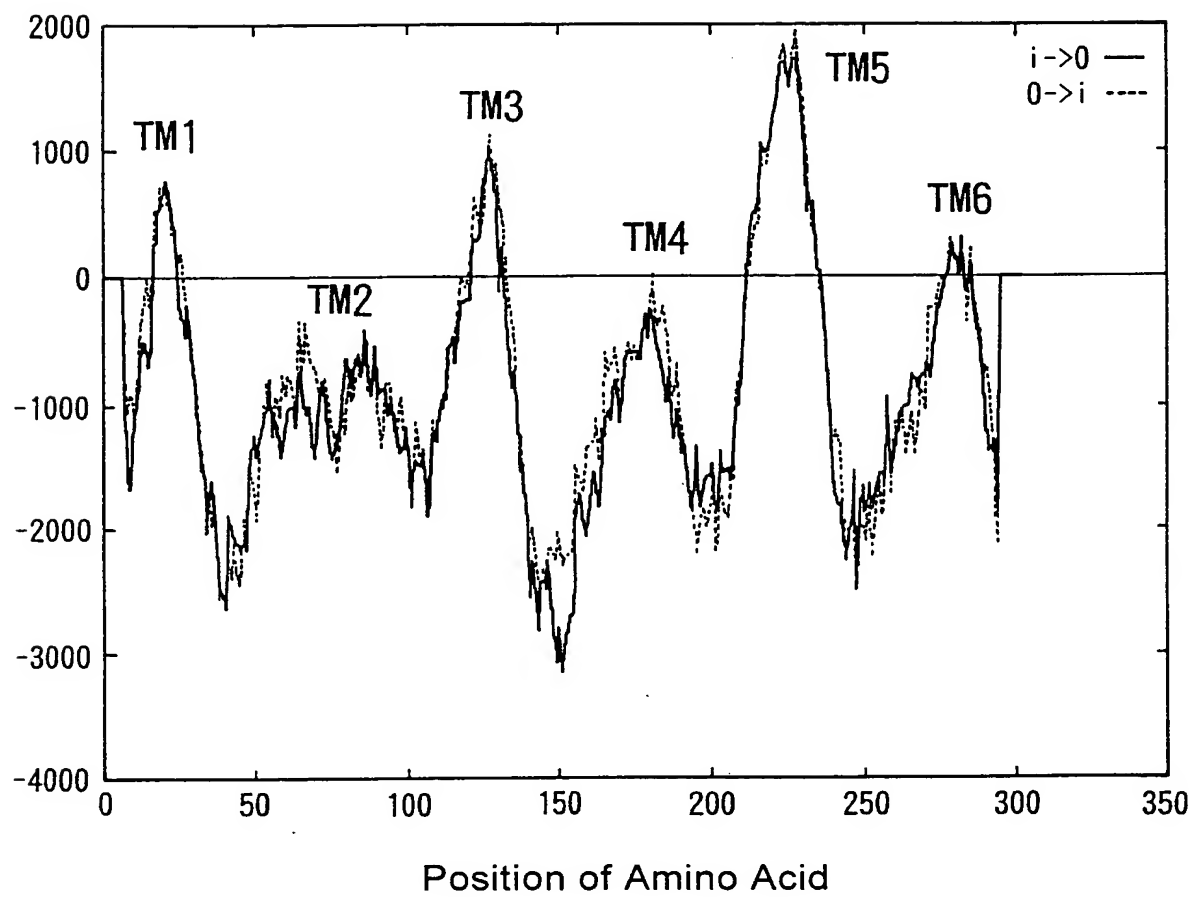


Fig.5

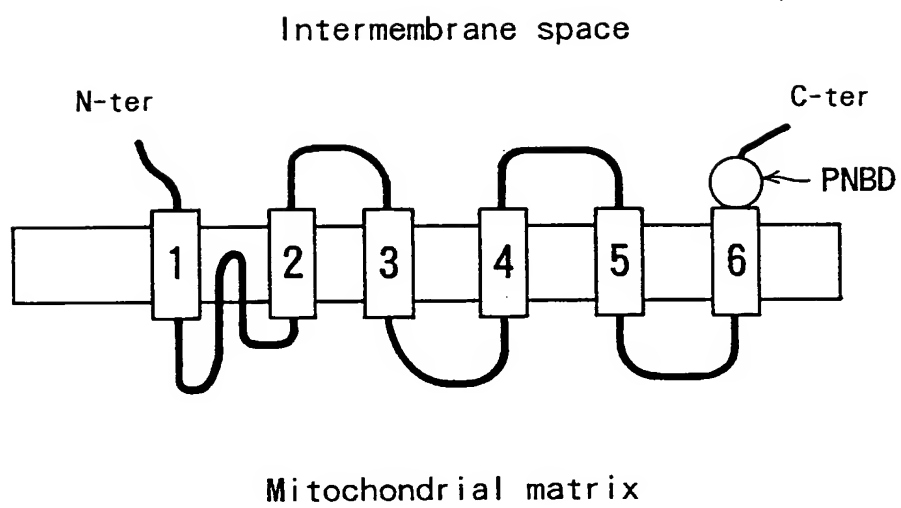


Fig.6

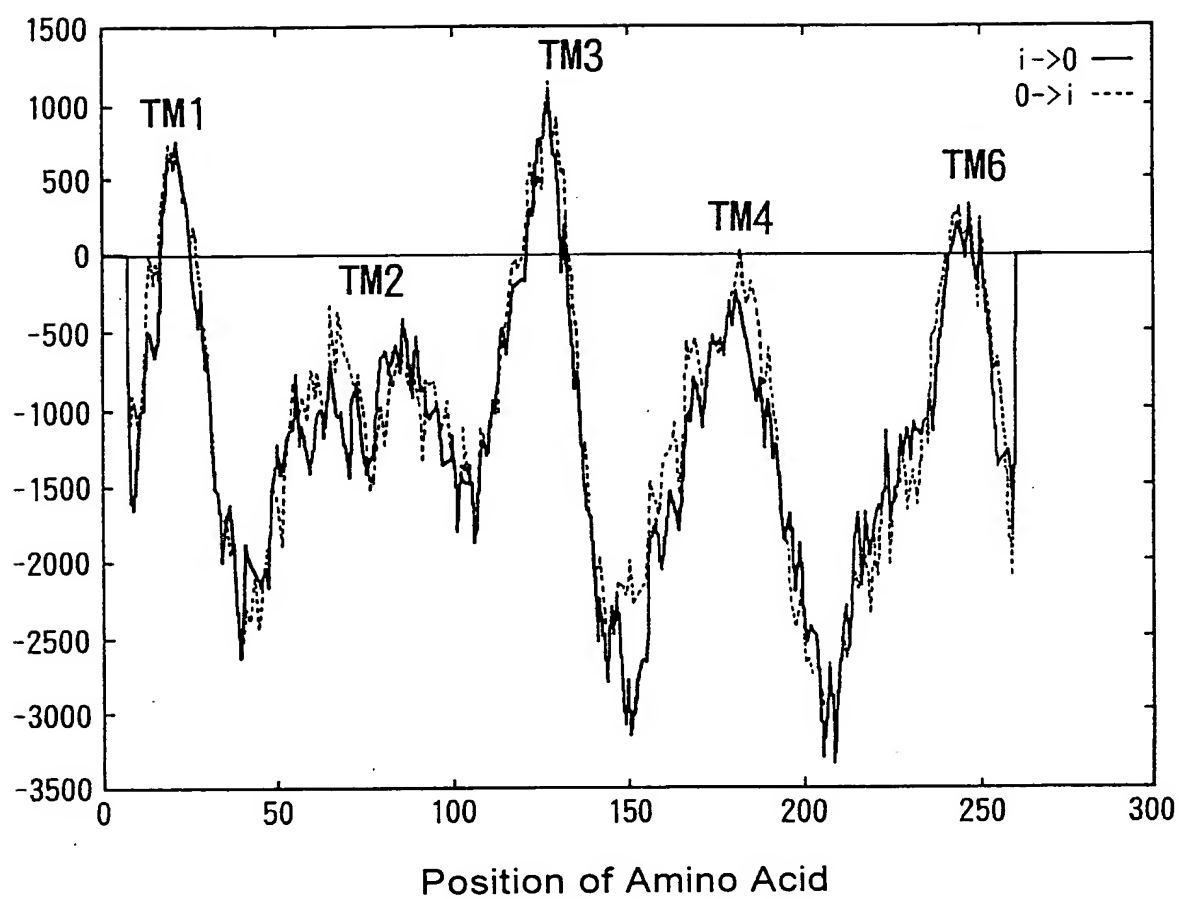


Fig.7

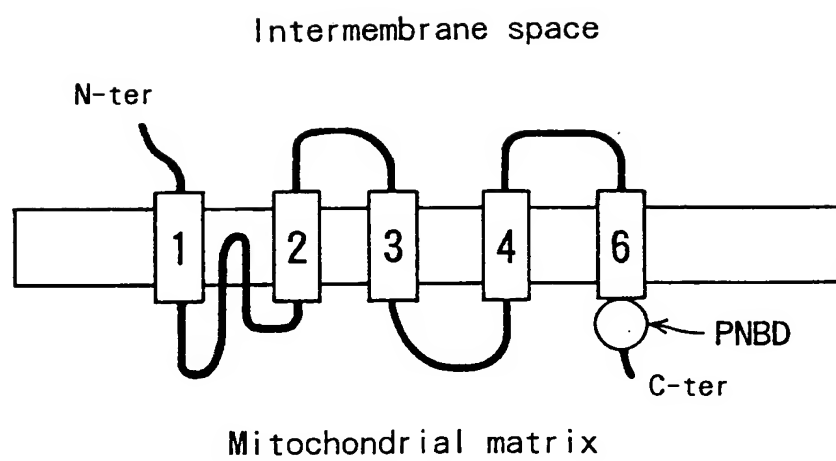


Fig.8

